

CRF Errors Corrected by the STIC Systems Branch

5040 01PE

Serial Number: 10/088,0

Processing Date: 4/4/02

Entered by: DC (STIC staff)

#5

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☒ other invalid text, such as "primer" in Seq. ID 5 in the <213.7 field
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95



Does Not Comply OIPE
Corrected Diskette Needed

Errors on p. 5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,045

DATE: 04/04/2002

TIME: 15:17:37

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\04042002\J088045.raw

```

4 <110> APPLICANT: Joelle Thonnard
6 <120> TITLE OF INVENTION: Novel Compounds
9 <130> FILE REFERENCE: BM45412
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/088,045
C--> 11 <141> CURRENT FILING DATE: 2002-03-14
11 <150> PRIOR APPLICATION NUMBER: 9921691.3
12 <151> PRIOR FILING DATE: 1999-09-14
14 <160> NUMBER OF SEQ ID NOS: 10
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1509
20 <212> TYPE: DNA
21 <213> ORGANISM: Moraxella catarrhalis
23 <400> SEQUENCE: 1
24 atgtctaagc ctactttgat aaaaacaacc ttaatttgtg cottaagtgc attgatgctc      60
25 agtggttgta gcaatcaagc ggacaaagcc gcccagccaa aaagcagcac ggtagacgct      120
26 gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct      180
27 gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac      240
28 cccgccaagc tgggtggtaaa aatggaaacc gttgaaaaag tcatgctgct gccagatggc      300
29 gtggaataac agttttggac atttggcggc caagttccag ggcagatgat tcgtgtgcgt      360
30 gaaggcgaca ccacggaagt gcagttctca aaccacccag attcaaaaat gcccataat      420
31 gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg      480
32 ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt      540
33 gcggttgccc ctggtggcat gcacattgct aatggcatgt atggtttgat tttggttgaa      600
34 ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat      660
35 accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga      720
36 gaagatgctg aatatgttgt ctttaattgt tcggtggggg cgttgactgg tgaaaatgct      780
37 ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg      840
38 acatcatcat tccatgtcat tggtgagatt tttgataagg ttcactttga gggtggtgaa      900
39 ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa      960
40 tttaagggtg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt      1020
41 aacaaagggg cattgggcat acttaagggt gaagggtgaag aaaatcatga gatttattca      1080
42 cacaaacaaa cagacgctgt ctatctgcca gaggggtgcc cacaagcaat tgatacccaa      1140
43 gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca      1200
44 acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct      1260
45 ttcccaccgc ttgccaaact tgactatctg aacgccgacc acgctcgtgc cgccagcatc      1320
46 gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatt      1380
47 cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc      1440
48 tttggttaaca aaggcgggtc actcagtgca gacgatgtgg caaaagccaa aaaaaccaag      1500
49 ccaaaactga                                     1509
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 502
53 <212> TYPE: PRT

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54 <213> ORGANISM: Moraxella catarrhalis

56 <400> SEQUENCE: 2

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57 Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser
58 1 5 10 15
59 Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
60 20 25 30
61 Pro Lys Ser Ser Thr Val Asp Ala Ala Ala Lys Thr Ala Asn Ala Asp
62 35 40 45
63 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
64 50 55 60
65 Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
66 65 70 75 80
67 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
68 85 90 95
69 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
70 100 105 110
71 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
72 115 120 125
73 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
74 130 135 140
75 Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
76 145 150 155 160
77 Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
78 165 170 175
79 Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
80 180 185 190
81 Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
82 195 200 205
83 Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
84 210 215 220
85 Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
86 225 230 235 240
87 Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
88 245 250 255
89 Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
90 260 265 270
91 Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
92 275 280 285
93 Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
94 290 295 300
95 Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
96 305 310 315 320
97 Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
98 325 330 335
99 Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
100 340 345 350
101 Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr
102 355 360 365
103 Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys

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104      370      375      380
105 Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
106 385      390      395      400
107 Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
108      405      410      415
109 Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
110      420      425      430
111 Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
112      435      440      445
113 Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
114      450      455      460
115 Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
116 465      470      475      480
117 Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
118      485      490      495
119 Lys Lys Thr Lys Pro Asn
120      500
122 <210> SEQ ID NO: 3
123 <211> LENGTH: 1506
124 <212> TYPE: DNA
125 <213> ORGANISM: Moraxella catarrhalis
127 <400> SEQUENCE: 3
128 atgtctaagc ctactttgat aaaaacaacc ttaatttgtg cettaagtgc attgatgctc 60
129 agtggttgta gcaatcaagc ggacaaagcc gccagccaa aaagcagcac ggtagacgct 120
130 gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct 180
131 gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac 240
132 cccgccaatg tgggtggtaaa aatggaaacc gttgaaaaag tcatgctgtc gccagatggc 300
133 gtggaataat agttttggac atttggcggt caagttccag ggcagatgat tcgtgtgcgt 360
134 gaaggcgaca ccattcgaagt gcagtcttca aaccaccag attcaaaaat gcccataat 420
135 gttgactttc acgctgccac agggcctggc ggcgggggcag aagcgtcatt taccgcaccg 480
136 ggtcatacat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt 540
137 gcggttgccc ctgttgccat gcacattgct aatggcatgt atggtttgat tttggttgaa 600
138 ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat 660
139 accaaaggca aatatggcga acaagggtcta cagccctttg atatggaaaa agccattcga 720
140 gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct 780
141 ctaaaagcca aggttggcga aactgttcgc ttatttgtgg gtaacggcgg cccgaatttg 840
142 acatcatcat tccatgtcat tggtagagatt ttgataagg ttcaacttga ggggtggtaa 900
143 ggtgaaaacc acaatatcca aaccacgcta atcccagcag gtggcgctgc catcactgaa 960
144 ttttaagggtg atgtgccggg tgattatgtc ttggttgacc atgccatctt ccgtgccttt 1020
145 aacaaagggg cattgggcat acttaagggt gaagggtgaag aaaatcatga gatttattca 1080
146 cacaacaaa cagacgtgtg ctatctgcc aagggtgccc cacaagcaat tgatacccaa 1140
147 gaagcaccga aaacacctgc acctgccaac ttacaagagc agattaaagc aggttaaggca 1200
148 acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct 1260
149 ttcccaccgc ttgccaaact tgactatctg aacgccgacc acgctcgtgc cgccagcatc 1320
150 gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg 1380
151 cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc 1440
152 tttggtaaca aaggcggtca actcagtgc gacgatgtgg caaaagccaa aaaaaccaag 1500
153 ccaaac
155 <210> SEQ ID NO: 4

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156 <211> LENGTH: 502

157 <212> TYPE: PRT

158 <213> ORGANISM: Moraxella catarrhalis

160 <400> SEQUENCE: 4

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161 Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser
162 1 5 10 15
163 Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln
164 20 25 30
165 Pro Lys Ser Ser Thr Val Asp Ala Ala Lys Thr Ala Asn Ala Asp
166 35 40 45
167 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala
168 50 55 60
169 Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His
170 65 70 75 80
171 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg
172 85 90 95
173 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val
174 100 105 110
175 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln
176 115 120 125
177 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His
178 130 135 140
179 Ala Ala Thr Gly Pro Gly Gly Gly Ala Glu Ala Ser Phe Thr Ala Pro
180 145 150 155 160
181 Gly His Thr Ser Thr Phe Ser Phe Lys Ala Leu Gln Pro Gly Leu Tyr
182 165 170 175
183 Val Tyr His Cys Ala Val Ala Pro Val Gly Met His Ile Ala Asn Gly
184 180 185 190
185 Met Tyr Gly Leu Ile Leu Val Glu Pro Lys Glu Gly Leu Pro Lys Val
186 195 200 205
187 Asp Lys Glu Tyr Tyr Val Met Gln Gly Asp Phe Tyr Thr Lys Gly Lys
188 210 215 220
189 Tyr Gly Glu Gln Gly Leu Gln Pro Phe Asp Met Glu Lys Ala Ile Arg
190 225 230 235 240
191 Glu Asp Ala Glu Tyr Val Val Phe Asn Gly Ser Val Gly Ala Leu Thr
192 245 250 255
193 Gly Glu Asn Ala Leu Lys Ala Lys Val Gly Glu Thr Val Arg Leu Phe
194 260 265 270
195 Val Gly Asn Gly Gly Pro Asn Leu Thr Ser Ser Phe His Val Ile Gly
196 275 280 285
197 Glu Ile Phe Asp Lys Val His Phe Glu Gly Gly Lys Gly Glu Asn His
198 290 295 300
199 Asn Ile Gln Thr Thr Leu Ile Pro Ala Gly Gly Ala Ala Ile Thr Glu
200 305 310 315 320
201 Phe Lys Val Asp Val Pro Gly Asp Tyr Val Leu Val Asp His Ala Ile
202 325 330 335
203 Phe Arg Ala Phe Asn Lys Gly Ala Leu Gly Ile Leu Lys Val Glu Gly
204 340 345 350
205 Glu Glu Asn His Glu Ile Tyr Ser His Lys Gln Thr Asp Ala Val Tyr

```

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```

206          355          360          365
207 Leu Pro Glu Gly Ala Pro Gln Ala Ile Asp Thr Gln Glu Ala Pro Lys
208          370          375          380
209 Thr Pro Ala Pro Ala Asn Leu Gln Glu Gln Ile Lys Ala Gly Lys Ala
210 385          390          395          400
211 Thr Tyr Asp Ser Asn Cys Ala Ala Cys His Gln Pro Asp Gly Lys Gly
212          405          410          415
213 Val Pro Asn Ala Phe Pro Pro Leu Ala Asn Ser Asp Tyr Leu Asn Ala
214          420          425          430
215 Asp His Ala Arg Ala Ala Ser Ile Val Ala Asn Gly Leu Ser Gly Lys
216          435          440          445
217 Ile Thr Val Asn Gly Asn Gln Tyr Glu Ser Val Met Pro Ala Ile Ala
218          450          455          460
219 Leu Ser Asp Gln Gln Ile Ala Asn Val Ile Thr Tyr Thr Leu Asn Ser
220 465          470          475          480
221 Phe Gly Asn Lys Gly Gly Gln Leu Ser Ala Asp Asp Val Ala Lys Ala
222          485          490          495
223 Lys Lys Thr Lys Pro Asn
224          500

```

226 <210> SEQ ID NO: 5

227 <211> LENGTH: 21

228 <212> TYPE: DNA

C--> 229 <213> ORGANISM: primer Artificial Sequence *delete*

231 <220> FEATURE:

232 <223> OTHER INFORMATION: primer

234 <400> SEQUENCE: 5

235 aagcgaacag ttctgccaac c

21

237 <210> SEQ ID NO: 6

238 <211> LENGTH: 23

239 <212> TYPE: DNA

240 <213> ORGANISM: Artificial Sequence

242 <220> FEATURE:

243 <223> OTHER INFORMATION: primer

245 <400> SEQUENCE: 6

246 gggggcggttg actggtgaaa atg

23

248 <210> SEQ ID NO: 7

249 <211> LENGTH: 17

250 <212> TYPE: DNA

251 <213> ORGANISM: Artificial Sequence

253 <220> FEATURE:

254 <223> OTHER INFORMATION: primer

256 <400> SEQUENCE: 7

257 gtaaaacgac ggccagt

17

259 <210> SEQ ID NO: 8

260 <211> LENGTH: 17

261 <212> TYPE: DNA

262 <213> ORGANISM: Artificial Sequence

264 <220> FEATURE:

265 <223> OTHER INFORMATION: primer

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:229 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5